



wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 12:53 pm BST

PDB ID : 5Y9E
Title : Crystal structure of HPV58 pentamer
Authors : Li, S.W.; Li, Z.H.
Deposited on : 2017-08-24
Resolution : 2.04 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

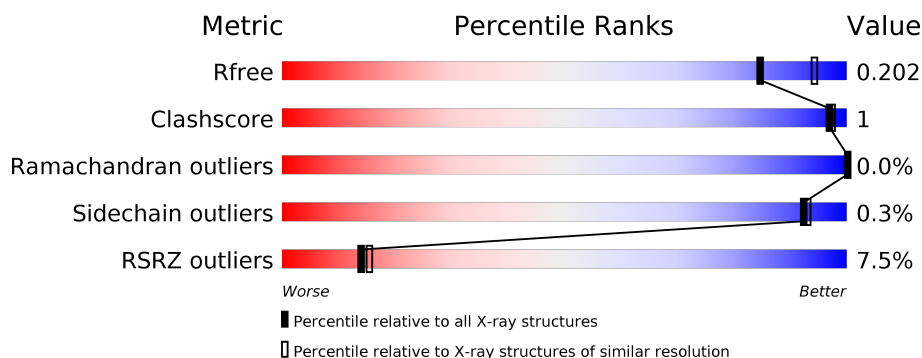
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	490	<div> <div>5%</div> <div> <div></div> <div>82%</div> <div>•</div> <div>15%</div> </div> </div>
1	B	490	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>•</div> <div>16%</div> </div> </div>
1	C	490	<div> <div>7%</div> <div> <div></div> <div>83%</div> <div>•</div> <div>15%</div> </div> </div>
1	D	490	<div> <div>7%</div> <div> <div></div> <div>84%</div> <div>•</div> <div>15%</div> </div> </div>
1	E	490	<div> <div>9%</div> <div> <div></div> <div>83%</div> <div>•</div> <div>14%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	B	501	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17883 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Major capsid protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	0	1	0
			3323	2120	551	632	20			
1	B	414	Total	C	N	O	S	0	1	0
			3312	2114	549	629	20			
1	C	415	Total	C	N	O	S	0	1	0
			3318	2117	550	631	20			
1	D	418	Total	C	N	O	S	0	1	0
			3332	2125	554	633	20			
1	E	420	Total	C	N	O	S	0	1	0
			3348	2133	558	637	20			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	MET	-	initiating methionine	UNP P26535
A	176	SER	CYS	engineered mutation	UNP P26535
B	9	MET	-	initiating methionine	UNP P26535
B	176	SER	CYS	engineered mutation	UNP P26535
C	9	MET	-	initiating methionine	UNP P26535
C	176	SER	CYS	engineered mutation	UNP P26535
D	9	MET	-	initiating methionine	UNP P26535
D	176	SER	CYS	engineered mutation	UNP P26535
E	9	MET	-	initiating methionine	UNP P26535
E	176	SER	CYS	engineered mutation	UNP P26535

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	6	Total	Mg	0	0
			6	6		
3	A	7	Total	Mg	0	0
			7	7		
3	D	6	Total	Mg	0	0
			6	6		
3	C	6	Total	Mg	0	0
			6	6		
3	E	4	Total	Mg	0	0
			4	4		

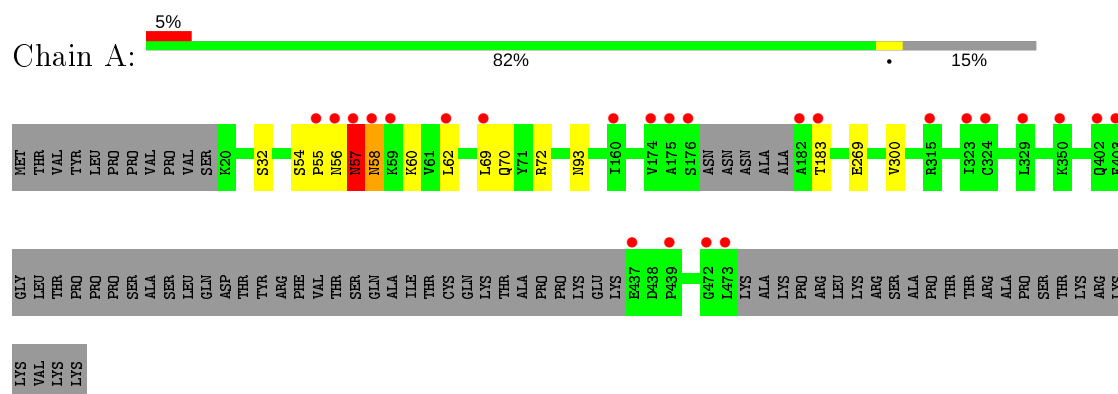
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	250	Total	O	0	0
			250	250		
4	B	238	Total	O	0	0
			238	238		
4	C	231	Total	O	0	0
			231	231		
4	D	205	Total	O	0	0
			205	205		
4	E	177	Total	O	0	0
			177	177		

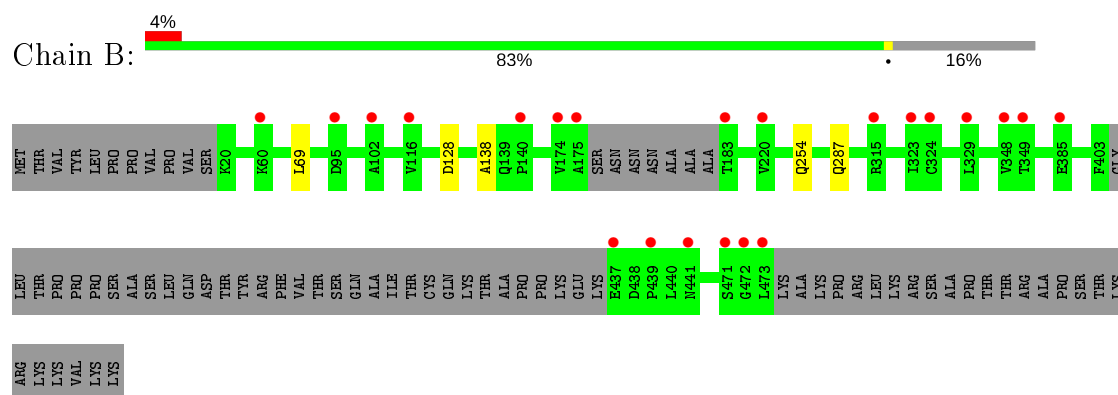
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

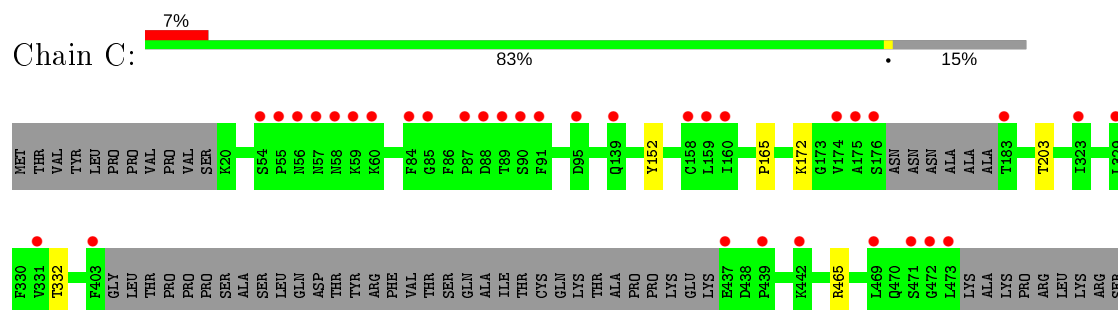
• Molecule 1: Major capsid protein L1



• Molecule 1: Major capsid protein L1

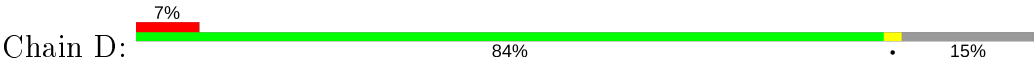


• Molecule 1: Major capsid protein L1



ALA
PRO
THR
THR
THR
ARG
ALA
PRO
SER
THR
LYS
ARG
LYS
LYS
VAL
LYS

● Molecule 1: Major capsid protein L1

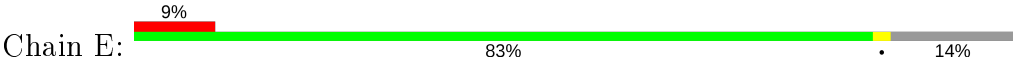


MET THR VAL TYR LEU PRO PRO VAL SER ASP THR K20 S51 S54 P55 N56 N57 N58 K59 K60 Q70 Y71 Y72 P87 D88 A102 G111 Q112 V174 A175 S176 ASN ASN N179 A180 A181 A182 T183 R315 I323 C324 L329 T340 E385 I386 M387 F403

GLY LEU THR PRO PRO PRO SER ALA SER LEU GLN ASP THR THR ARG PHE VAL THR SER GLN ALA ILE THR CYS GLN LYS THR ALA PRO PRO LYS GLU LYS D438 P439 L440 M441 K442 S471 Q472 L473 LYS ALA LYS PRO ARG LEU LYS ARG SER LYS THR PRO THR ARG ALA PRO SER

THR
LYS
ARG
LYS
VAL
LYS
LYS

● Molecule 1: Major capsid protein L1



MET THR VAL TYR LEU PRO PRO VAL SER ASP THR K20 Y21 S54 P55 N56 N57 N58 K59 K60 V61 L62 Q70 Y71 Y72 G85 F86 P87 D88 T89 S90 T96 G103 Q139 G161 G174 A175 S176 A180 A181 A182 T183 D184 E269 K309 R315 I323

C324 L329 L382 T383 A384 E385 F403 GLY LEU THR PRO PRO ARG PHE VAL THR THR CYS GLN LYS THR ALA PRO PRO LYS GLU LYS D438 P439 L440 M441 Y443 E452 S471 Q472 L473 LYS ALA LYS PRO

ARG
LEU
LYS
ARG
SER
ALA
PRO
THR
THR
ARG
ALA
PRO
SER
THR
LYS
ARG
LYS
LYS
VAL
LYS
LYS

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	187.21Å 101.80Å 136.19Å 90.00° 95.68° 90.00°	Depositor
Resolution (Å)	29.78 – 2.04 29.78 – 2.04	Depositor EDS
% Data completeness (in resolution range)	98.9 (29.78-2.04) 98.9 (29.78-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.43 (at 2.04Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575)	Depositor
R, R_{free}	0.168 , 0.198 0.173 , 0.202	Depositor DCC
R_{free} test set	12229 reflections (7.67%)	wwPDB-VP
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.906	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	17883	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.26	0/3412	0.46	0/4627
1	B	0.26	0/3401	0.46	0/4612
1	C	0.25	0/3407	0.45	0/4620
1	D	0.25	0/3421	0.45	0/4640
1	E	0.25	0/3438	0.45	0/4665
All	All	0.25	0/17079	0.45	0/23164

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3323	0	3204	9	1
1	B	3312	0	3194	3	0
1	C	3318	0	3199	5	0
1	D	3332	0	3214	4	1
1	E	3348	0	3227	7	0
2	A	24	0	32	0	0
2	B	30	0	40	0	0
2	C	18	0	24	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	24	0	32	1	0
2	E	24	0	32	0	0
3	A	7	0	0	0	0
3	B	6	0	0	0	0
3	C	6	0	0	0	0
3	D	6	0	0	0	0
3	E	4	0	0	0	0
4	A	250	0	0	1	0
4	B	238	0	0	1	0
4	C	231	0	0	2	0
4	D	205	0	0	2	0
4	E	177	0	0	3	0
All	All	17883	0	16198	28	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

The worst 5 of 28 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:20:LYS:N	4:E:601:HOH:O	2.15	0.79
1:A:70:GLN:OE1	1:A:72:ARG:NH2	2.17	0.77
1:E:70:GLN:OE1	1:E:72:ARG:NH2	2.17	0.77
1:D:70:GLN:OE1	1:D:72:ARG:NH2	2.26	0.68
1:A:55:PRO:HG2	1:A:62:LEU:HD22	1.80	0.63

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:ASN:ND2	1:D:55:PRO:O[3_445]	2.01	0.19

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	411/490 (84%)	397 (97%)	13 (3%)	1 (0%)	47	39
1	B	409/490 (84%)	397 (97%)	12 (3%)	0	100	100
1	C	410/490 (84%)	399 (97%)	11 (3%)	0	100	100
1	D	413/490 (84%)	400 (97%)	13 (3%)	0	100	100
1	E	417/490 (85%)	401 (96%)	16 (4%)	0	100	100
All	All	2060/2450 (84%)	1994 (97%)	65 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	371/435 (85%)	368 (99%)	3 (1%)	81	82
1	B	370/435 (85%)	369 (100%)	1 (0%)	92	93
1	C	371/435 (85%)	371 (100%)	0	100	100
1	D	371/435 (85%)	371 (100%)	0	100	100
1	E	373/435 (86%)	372 (100%)	1 (0%)	92	93
All	All	1856/2175 (85%)	1851 (100%)	5 (0%)	92	93

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	58	ASN
1	A	69	LEU
1	B	69	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	59	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 49 ligands modelled in this entry, 29 are monoatomic - leaving 20 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GOL	D	503	-	5,5,5	0.34	0	5,5,5	0.22	0
2	GOL	A	503	-	5,5,5	0.35	0	5,5,5	0.26	0
2	GOL	C	503	-	5,5,5	0.39	0	5,5,5	0.09	0
2	GOL	B	504	-	5,5,5	0.38	0	5,5,5	0.21	0
2	GOL	B	503	-	5,5,5	0.37	0	5,5,5	0.26	0
2	GOL	E	502	-	5,5,5	0.36	0	5,5,5	0.21	0
2	GOL	D	504	-	5,5,5	0.35	0	5,5,5	0.16	0
2	GOL	A	502	-	5,5,5	0.38	0	5,5,5	0.17	0
2	GOL	C	502	-	5,5,5	0.38	0	5,5,5	0.18	0
2	GOL	E	501	-	5,5,5	0.38	0	5,5,5	0.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	B	505	-	5,5,5	0.37	0	5,5,5	0.24	0
2	GOL	C	501	-	5,5,5	0.37	0	5,5,5	0.18	0
2	GOL	D	501	3	5,5,5	0.39	0	5,5,5	0.16	0
2	GOL	A	501	-	5,5,5	0.39	0	5,5,5	0.14	0
2	GOL	B	501	-	5,5,5	0.37	0	5,5,5	0.24	0
2	GOL	D	502	-	5,5,5	0.39	0	5,5,5	0.23	0
2	GOL	A	504	-	5,5,5	0.38	0	5,5,5	0.20	0
2	GOL	B	502	-	5,5,5	0.37	0	5,5,5	0.20	0
2	GOL	E	503	-	5,5,5	0.38	0	5,5,5	0.16	0
2	GOL	E	504	-	5,5,5	0.38	0	5,5,5	0.13	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	D	503	-	-	2/4/4/4	-
2	GOL	A	503	-	-	0/4/4/4	-
2	GOL	C	503	-	-	4/4/4/4	-
2	GOL	B	504	-	-	2/4/4/4	-
2	GOL	B	503	-	-	2/4/4/4	-
2	GOL	E	502	-	-	2/4/4/4	-
2	GOL	D	504	-	-	2/4/4/4	-
2	GOL	A	502	-	-	2/4/4/4	-
2	GOL	C	502	-	-	2/4/4/4	-
2	GOL	E	501	-	-	2/4/4/4	-
2	GOL	B	505	-	-	2/4/4/4	-
2	GOL	C	501	-	-	1/4/4/4	-
2	GOL	D	501	3	-	4/4/4/4	-
2	GOL	A	501	-	-	2/4/4/4	-
2	GOL	B	501	-	-	2/4/4/4	-
2	GOL	D	502	-	-	2/4/4/4	-
2	GOL	A	504	-	-	3/4/4/4	-
2	GOL	B	502	-	-	2/4/4/4	-
2	GOL	E	503	-	-	2/4/4/4	-
2	GOL	E	504	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	502	GOL	O1-C1-C2-C3
2	B	502	GOL	O1-C1-C2-C3
2	E	503	GOL	O1-C1-C2-C3
2	E	504	GOL	O1-C1-C2-C3
2	D	501	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	504	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	416/490 (84%)	0.13	24 (5%)	23	25	25, 39, 76, 125	0
1	B	414/490 (84%)	0.06	22 (5%)	26	28	27, 41, 69, 101	0
1	C	415/490 (84%)	0.29	34 (8%)	11	12	30, 43, 84, 118	0
1	D	418/490 (85%)	0.29	33 (7%)	12	13	30, 46, 81, 125	0
1	E	420/490 (85%)	0.33	44 (10%)	6	6	28, 46, 86, 120	0
All	All	2083/2450 (85%)	0.22	157 (7%)	14	15	25, 43, 81, 125	0

The worst 5 of 157 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	181	ALA	7.7
1	C	175	ALA	7.5
1	C	473	LEU	7.3
1	D	175	ALA	7.3
1	D	473	LEU	6.9

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GOL	B	501	6/6	0.42	0.43	100,103,106,107	0
2	GOL	E	503	6/6	0.43	0.32	79,80,82,86	0
2	GOL	B	505	6/6	0.45	0.33	131,134,134,135	0
2	GOL	E	504	6/6	0.54	0.35	81,84,86,86	0
2	GOL	C	503	6/6	0.55	0.28	85,87,88,89	0
2	GOL	C	502	6/6	0.58	0.23	78,83,85,86	0
2	GOL	B	503	6/6	0.62	0.30	85,91,93,95	0
2	GOL	C	501	6/6	0.64	0.25	86,88,90,90	0
2	GOL	D	504	6/6	0.66	0.24	65,78,80,81	0
2	GOL	D	502	6/6	0.71	0.32	78,82,86,86	0
2	GOL	D	503	6/6	0.74	0.38	60,67,68,72	0
3	MG	A	510	1/1	0.75	0.27	76,76,76,76	0
3	MG	C	505	1/1	0.78	0.28	58,58,58,58	0
2	GOL	A	502	6/6	0.78	0.18	81,83,86,86	0
3	MG	E	507	1/1	0.78	0.20	64,64,64,64	0
2	GOL	B	504	6/6	0.79	0.25	71,74,76,77	0
2	GOL	A	503	6/6	0.79	0.38	58,60,62,64	0
2	GOL	A	504	6/6	0.80	0.19	54,60,62,62	0
3	MG	A	508	1/1	0.82	0.15	65,65,65,65	0
2	GOL	E	502	6/6	0.82	0.25	58,67,69,71	0
3	MG	D	508	1/1	0.82	0.46	72,72,72,72	0
2	GOL	B	502	6/6	0.84	0.18	92,92,94,94	0
3	MG	C	508	1/1	0.84	0.12	91,91,91,91	0
2	GOL	A	501	6/6	0.85	0.28	38,62,69,71	0
2	GOL	E	501	6/6	0.85	0.27	72,73,74,75	0
3	MG	D	510	1/1	0.87	0.07	63,63,63,63	0
3	MG	B	509	1/1	0.87	0.54	62,62,62,62	0
3	MG	A	507	1/1	0.88	0.13	69,69,69,69	0
3	MG	D	506	1/1	0.89	0.15	50,50,50,50	0
3	MG	B	511	1/1	0.89	0.34	67,67,67,67	0
3	MG	C	509	1/1	0.89	0.13	60,60,60,60	0
2	GOL	D	501	6/6	0.90	0.16	33,59,66,71	0
3	MG	B	506	1/1	0.91	0.15	52,52,52,52	0
3	MG	C	507	1/1	0.92	0.25	55,55,55,55	0
3	MG	C	506	1/1	0.93	0.14	56,56,56,56	0
3	MG	A	509	1/1	0.93	0.15	45,45,45,45	0
3	MG	A	505	1/1	0.94	0.15	42,42,42,42	0
3	MG	A	511	1/1	0.94	0.09	45,45,45,45	0
3	MG	E	505	1/1	0.94	0.07	61,61,61,61	0
3	MG	B	508	1/1	0.94	0.20	50,50,50,50	0
3	MG	A	506	1/1	0.95	0.09	42,42,42,42	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MG	B	510	1/1	0.95	0.10	46,46,46,46	0
3	MG	D	507	1/1	0.95	0.49	66,66,66,66	0
3	MG	E	506	1/1	0.97	0.28	59,59,59,59	0
3	MG	B	507	1/1	0.97	0.12	52,52,52,52	0
3	MG	D	509	1/1	0.97	0.15	60,60,60,60	0
3	MG	D	505	1/1	0.97	0.09	46,46,46,46	0
3	MG	E	508	1/1	0.97	0.09	58,58,58,58	0
3	MG	C	504	1/1	0.98	0.06	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.